AMENDMENTS TO THE SPECIFICATION

Please amend the specification as follows.

Delete Tables 1-9 and 11.

Delete paragraphs 0035-0082.

Add the following paragraphs after 0034.

> The present invention relates to an isolated nucleic acid selected from the group consisting of (a) SEQ ID NO: 6527, (b) a DNA encoding the nucleic acid of (a), wherein the DNA is identical in length to (a); and (c) the complement of (a) or (b), wherein the complement is identical in length to the nucleic acid of (a) or (b). Additionally, the present invention relates to vectors or probes comprising a human insert, wherein the human insert consists of the nucleic acid selected from the group consisting of (a) SEQ ID NO: 6527, (b) a DNA encoding the nucleic acid of (a), wherein the DNA is identical in length to (a); and (c) the complement of (a) or (b), wherein the complement is identical in length to the nucleic acid of (a) or (b), and wherein the vector or probe comprises no other insert but the nucleic acid as described above.
>
> The present invention also relates to an isolated nucleic acid selected from the group consisting of (a) SEQ ID NO: 15, (b) a DNA encoding the nucleic acid of (a), wherein the DNA is identical in length to (a); and (c) the complement of (a) or (b), wherein the complement is identical in length to the nucleic acid of (a) or (b). Additionally, the present invention relates to vectors or probes comprising a human insert, wherein the human insert consists of the nucleic acid selected from the group consisting of (a) SEQ ID NO: 15, (b) a DNA encoding the nucleic acid of (a), wherein the DNA is identical in length to (a); and (c) the complement of (a) or (b), wherein the complement is identical in length to the nucleic acid of (a) or (b), and wherein the vector or probe comprises no other insert but the nucleic acid as described above.

Delete paragraphs 0156-0161.

Add the following paragraphs and tables after paragraph 0155.

The nucleotide sequence of the predicted human GAM RNA (miRNA) GAM1032, which is described by Fig. 8, and its respective genomic source and genomic location are set forth in Tables 1-3. Table 1 describes the predicted human GAM RNA (miRNA) as set forth in SEQ ID NO: 15.

Table 1

GAM SEQ-ID	GAM NAME	GAM RNA SEQUENCE	GAM POS
15	GAM1032	CTAGACTGAAGCTCCTTGAGGA	A

Table 2 describes the GAM PRECURSOR RNA (hairpin) as set forth in SEQ ID NO: 6527 and how it relates to Fig. 8.

Table 2

GAM NAME	PRECUR SEQ-ID	PRECURSOR SEQUENCE	GAM DESCRIPTION
GAM1032	6527	GCTAGTCACT GGGGCAAAGA TGACTAAAAC ACTTTTCCTG CCCTCGAGGA GCTCACAGTC TAGTATGTCT CATCCCCTAC TAGACTGAAG CTCCTTGAGG ACAGGGATGG TCATACTCAC CTCGGTGTTG C	Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 1032 (GAM1032) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art GAM1032 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM1032 was detected is described with additional reference to Figs. 9-15 GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome GAM1032 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1032 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1032 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1032 precursor RNA is designated SEQ ID:6527, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6527 is located from position 141427052 to position 141427182 relative to

chromosome 8 on the `-` strand. GAM1032 precursor RNA folds onto itself, forming GAM1032 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.Nucleotide sequence of GAM1032 precursor RNA, designated SEQ ID NO: 6527, and a schematic representation of a predicted secondary folding of GAM1032 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein An enzyme complex designated DICER COMPLEX, `dices` the GAM1032 folded precursor RNA yielding a GAM1032 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art,`dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1032 RNA, hereby incorporated herein. Expression of GAM1032 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24 GAM1032 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1032 target RNA, herein designated GAM TARGET RNA.GAM1032 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3`untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively GAM1032 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1032 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the

nucleotide sequence of GAM1032 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region,these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR region The complementary binding of GAM1032 RNA, herein designated GAM RNA, to target binding sites on GAM1032 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1032 target RNA into GAM1032 target protein, herein designated GAM TARGET PROTEIN, which is shown surrounded by a broken line It is appreciated that GAM1032 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1032 target genes. The mRNA of each one of this plurality of GAM1032 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1032 RNA, herein designated GAM RNA, and which when bound by GAM1032 RNA causes inhibition of translation of the GAM1032 target mRNA into a corresponding GAM1032 target protein.The mechanism of the translational inhibition exerted by GAM1032 RNA, herein designated GAM RNA,on one or more GAM1032 target genes,herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes Nucleotide sequence of GAM1032 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1032 folded precursor RNA, herein designated GAM FOLDED

PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein. Nucleotide sequences of a `diced` GAM1032 RNA, herein designated GAM RNA, of GAM1032 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1032 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1032 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.It is appreciated that specific functions, and accordingly utilities, of GAM1032 RNA correlate with, and may be deduced from, the identity of the GAM1032 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

Table 3 shows data relating to the source and location of the GAM oligonucleotide, specifically the GAM PRECURSOR (hairpin) and its position in the human genome.

Table 3

GAM NAME	PRECUR SEQ-ID	ORGANISM	CHR	STR AND	CHR-START OFFSET	CHR-END OFFSET	SOURCE REF-ID
GAM 1032	6527	hsa	8	-	141427052	141427182	

Table 4 shows a schematic representation of the GAM folded precursor as set forth in SEQ ID NO: 6527, beginning at the 5' end (beginning of upper row) to the 3' end (beginning of lower row), where the hairpin loop is positioned at the right part of the schematic.

Table 4

GAM NAME	PREC UR -SEQ ID	PRECURSOR GAM FOLDED PRECURSOR RNA -SEQUENCE

```
===  === =========  ========================

GAM   65 GCTAGTCACT  TAGT         CAAAG       AAACACTT      C            CA
1032  27 GGGGCAAAGA           TGT GC    CACTGGGG     ATGACTA         TTCCTG CCTCGAGGAGCT
         TGACTAAAAC  CAGTCTAGTA CG    GTGGCTCC     TACTGGT         AGGGAC GGAGTTCCTCGA
         ACTTTTCCTG  GTCAGATCAT   TT--         ACTCA       --------      A
         CCCTCGAGGA            A-          -- CTCATCCCC   ---------
         GCTCACAGTC
         TAGTATGTCT
         CATCCCCTAC
         TAGACTGAAG
         CTCCTTGAGG
         ACAGGGATGG
         TCATACTCAC
         CTCGGTGTTG
         C
```

Table 5 shows the mature GAM RNA as set forth in SEQ ID NO: 15 as sliced by DICER from the GAM PRECURSOR sequence (hairpin) as set forth in SEQ ID NO: 6527.

Table 5

GAM NAME	GAM RNA SEQUENCE	PRECUR SEQ-ID	SOURCE REF-ID	GAM POS
GAM1032	CTAGACTGAAGCTCCTTGAGGA	6527		A

Table 6 shows data relating to the SEQ ID NO of the GAM target binding site sequence of the target gene name as bound by the GAM RNA as set forth in SEQ ID NO: 15.

Table 6

TARGET BINDING SITE SEQ-ID	TARGET	TARGET BINDING SITE SEQUENCE
3504	CHAT	TGCTCCTGCCACTAGGTTTCA
3505	CHAT	TGGGGAAGTGCGGTGACTGGGAAATGC
3506	CHAT	CCAGCGCACAGCCTGGGCAG
3507	CHAT	CATCCCTGCACCAGGACTCACCAAGA
3508	CHAT	CAAGACGCCCATCCTGGAAAAGGTCCC
3509	CHAT	AGGCAGCAGAGCCGAGGAGAGCAGGT
3510	CHAT	CGCGTCAGGCCCAGCGCACAGCCTG

3511	CHAT	GCACAGCCTGGGCAGCTCAGCCTG
3512	CHAT	GAGCTAGGGGCAGGAGGCATG
3513	CHAT	GAGAAAGGAGTAGGAGCCTAGCA
3514	CHAT	GCCTCAAGGGGTGCGGCCCTCTCAG
3515	CHAT	GCGTCAGGCCCAGCGCACAGCCTG
3516	CHAT	GCTCAGCCTGTCAGCTGAGCACGGGCG
3517	CHAT	GCTTTGAGAAAGGAGTAG
3518	CHAT	GGTGACTGGGAAATGCTGAG
3519	CHAT	GTCCGACCTCTGGAAATGT
3520	CHAT	GGCTCACACCCCCGCCCACAC
3651	CTSK	GCACCCTAGAGGACTAGGGTA
3652	CTSK	CTTCCACGATGGTGCAGTG
3653	CTSK	CTTCCTACTTTGCTTCTCTCCA
3654	CTSK	CTTCCCTTCTTTGCAC
3655	CTSK	CTGACTTCTCACTTCCTAAG
3656	CTSK	CCTACTTTGCTTCTCTCCA
3657	CTSK	CCTTCCTACTTTGCTTCTCTC
3658	CTSK	GTCTATGTTTTCTACTCCAA
3659	CTSK	GTACAGGTACAGGCTGGAGATT
3660	CTSK	CAGTGTAACGATGCACTTTGG
3661	CTSK	AATAAATCTAGCACCCCTGAT
3662	CTSK	TCTATTCATAAGTCTTTGGTACAAG
3663	CTSK	TCCTGCTCTTCCATTTCTTCC
3664	CTSK	TCCTACTTTGCTTCTCTCCA
3665	CTSK	TCCTCAAGGTAGAAATGTCTAT
3666	CTSK	TCCATCCTGCTCTTCCATTTCTTCCA
3667	CTSK	TGACTTCTCACTTCCTAAG
3668	CTSK	TCTTCCACGATGGTGCAGTG
3669	CTSK	TTGAAGCAGATGTGGTGA

3670	CTSK	TTGTCCCAGGGCTGATGCTGT
3671	CTSK	TTTCCAGCCGATCACTGGAGCT
4796	MPO	TTTATCCATAGACAGGGCCC
4797	MPO	TATTGAGCACCTACTACATGCA
4798	MPO	TCCTTGCCCTAGATGAGCCCAGC
4799	MPO	TCCTCACCCTGATTTCTTGCTT
4800	MPO	TCAGGTGAGCTGTGGAGGTGGGGTC
4801	MPO	GGAGAAGAGAGATGGGGGTTCC
4802	MPO	GGAGCACAGCTCAGGAACTAGA
4803	MPO	GGAGGTGGGGTCCTTGGAAGC
4804	MPO	GCTCCCCTTTTTCTTCCTCA
4805	MPO	GCTCAGGAACTAGACTGCCTG
4806	MPO	GCTGGGCTGTGTGGTTGACTT
4807	MPO	GCCCAGCCCTGTTCTGGGTGCAG
4808	MPO	GGGCCTGTTGCCCTTTCTGTACCA
4809	MPO	GGGAAGCCTCCTAAGGCCAGG
4810	MPO	GGCCAGGTAAGGGGGTGCAGCAGTGAG
4811	MPO	GGCTCCCCTTTTTCTTCCTCACCCT
4812	MPO	GGTGAGCTGTGGAGGTGGGG
4813	MPO	GAGCAAATTACCCTCCTTAAACAAGAG
4814	MPO	CTTGTAAATTACATCTGTCATGGTTT
4815	MPO	CCTCAAGGAGGTCTGG
4816	MPO	CCTCTGGTTCTTCATTTATTGAG
4817	MPO	CTGAGTATGTGGAAGGCAGCA
4818	MPO	CTGAGTATGTGGAAGGCAGCAGAGCGGA
4819	MPO	AGGGCCCACTTGTATCCTCTG
4820	MPO	ATCTGTGTCCTGGTTAGCAGAGC
4821	MPO	CAGCTCAGGAACTAGACTGCCT
4822	MPO	CCCTCAAGGAGGTCTGG

4823	MPO	ACAGCTCAGGAACTAGACTGCCT
4824	MPO	AGGCAGCAGAGCGGACTGGTGA
4825	MPO	AAGGCAGCAGAGCGGACTGGTGA
5322	SERPIN	TGAAGCTCTCACACGCACAG
5323	SERPIN	CAGTCTGGAGGGTCCTGGCC
5324	SERPIN	CATGTGTGGCCCTGTCTGCTTA
5325	SERPIN	CCCATGGACTCTTCAGTCTGG
5326	SERPIN	ATGTGTGGCCCTGTCTGCTTA
5327	SERPIN	AGTAGGAACTTGGAATGCAAG
5328	SERPIN	GAAGCTCTCACACGCACAG
5329	SERPIN	CCTGTGCACCGTAGTGGCCATGG
5330	SERPIN	CTCTTCAGTCTGGAGGGTCCTGG
5331	SERPIN	GCCCATGGACTCTTCAGTCTGG
5541	TNFRSF	GTGAAAAACAACAAATTCAGTTCTGA
5542	TNFRSF	GTGACACACAGGTGTTCAAAGACG
5543	TNFRSF	GGCAAGACTGCCCTTAGAAATTCTAG
5544	TNFRSF	GCGTATGACACATTGA
5545	TNFRSF	GCCAGCCCTGGCTGCCCAGGCGGAG
5546	TNFRSF	GACGCTTCTGGGGAGTGAGGGAA
5547	TNFRSF	GACAATGTCCAAGACACAGCAGA
5548	TNFRSF	CTTTGCCACCTCTCCATTTTTGCC
5549	TNFRSF	CTGCCCTTAGAAATTCTAGCC
5550	TNFRSF	CTGGCTCAAAACTACCTA
5551	TNFRSF	CGCAAGAGTGACACACAGGTGTTCA
5552	TNFRSF	ATGTCCAAGACACAGCAGAACAGA
5553	TNFRSF	ATGCAGAAAGCACAGAAAGGA
5554	TNFRSF	ATGTAAACTGTGAAGATAGTT
5555	TNFRSF	ATGGAAAGAAAGAAGCGTATGACACA
5556	TNFRSF	ATGGAAAGAAAGAAGCGTATGACACAT

5557	TNFRSF	ATTTAAATAAGGCTCTACCTC
5558	TNFRSF	ACAATGTCCAAGACACAGCAGA
5559	TNFRSF	TCCTCAAGGACATTACTAG
5560	TNFRSF	TCTCAGGCATCAAAAGCATTTTG
5561	TNFRSF	TCCAAGGATGTTTAAAATCTAGTTGG
5562	TNFRSF	TGGGTGAAGAGAAAGGAAGTACAGA
5563	TNFRSF	TCTTTCTCAGGCATCAAAAGCATT
5564	TNFRSF	TTGGGTGAAGAGAAAGGAAGTACAGA

Table 7, lines 1468-1501 shows data relating to target genes and binding site of GAM oligonucleotides.

Table 7

GAM NAME	GAM RNA SEQUENCE	TARGET	TARGET REF-ID		UTR TARGET BS-SEQ	BINDING-SITE DRAW (UPPER:GAM;LOWER:TARGET)	GAM POS
GAM1032	CTAGACTG AAG CTCCTTGA GGA	CHAT	NM_020984.1	5	GCCTCA AGGGGT G CGGCCC TCTCAG	- --- AA A CT AGA CTG GCTCCTTGAGG GA TCT GGC TGGGGAACTCC C CCC G- G	A
GAM1032	CTAGACTG AAG CTCCTTGA GGA	CTSK	NM_000396.2	3	TCCTCA AGGTAG A AATGTC TAT	C TGAAG - TAGAC CT CCTTGAGGA ATCTG GA GGAACTCCT T TAAA- T	A
GAM1032	CTAGACTG AAG CTCCTTGA GGA	MPO	NM_000250.1	5	CCCTCA AGGAGG T CTGG	TGAAG A CTAGAC CTCCTTGAGG GGTCTG GAGGAACTCC ----- C	A
GAM1032	CTAGACTG AAG CTCCTTGA GGA	MPO	NM_000250.1	5	CCTCAA GGAGGT C TGG	TGAAG CTAGAC CTCCTTGAGG GGTCTG GAGGAACTCC -----	A
GAM1032	CTAGACTG AAG CTCCTTGA	SERPINA 3	NM_001085.2	3	CCCATG GACTCT T	C- T A CTAGACTGAAG TCC TG GG GGTCTGACTTC AGG AC CC	A

	GGA				CAGTCT GG	TC T -	
GAM103 2	CTAGACTG AAG CTCCTTGA GGA	SERPI NA 3	NM_00 1085. 2	3	GCCCAT GGACTC T TCAGTC TGG	C- T A A CTAGACTGAAG TCC TG GG GGTCTGACTTC AGG AC CC TC T - G	A
GAM103 2	CTAGACTG AAG CTCCTTGA GGA	TNFRS F6	NM_15 2874. 1	3	TCCTCA AGGACA T TACTAG	AC AGC CTAG TGA TCCTTGAGGA GATC ATT AGGAACTCCT -- AC-	A

It is appreciated that the specific functions and accordingly the utilities a GAM oligonucleotide that is described by Fig. 8 is correlated with and may be deduced from the identity of the GAM TARGET GENES inhibited thereby, and whose functions are set forth in Table 8. Table 8 shows data relating to the function and utilities of GAM RNA as set forth in SEQ ID NO: 15.

Table 8

GAM NAME	TARGET	GAM RNA SEQUENCE	GAM FUNCTION	GAM POS	TAR DIS

GAM1032	TNFRSF6	CTAGACTG AAGCTCC TTGAGGA	TNFRSF6 (Accession NM_152874.1) is another GAM1032 target gene. TNFRSF6 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TNFRSF6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFRSF6 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1032 RNA are set forth in Tables 6 and 7, hereby incorporated herein. Another function of GAM1032 is therefore inhibition of TNFRSF6. Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFRSF6.	A	A
GAM1032	CHAT	CTAGACTG AAGCTCC TTGAGGA	Choline Acetyltransferase (CHAT, Accession NM_020984.1) is a GAM1032 target gene. CHAT BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CHAT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CHAT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1032 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A function of GAM1032 is therefore inhibition of	A	A

			CHAT, a GAM1032 target gene which synthesizes the neurotransmitter acetylcholine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CHAT.The function of CHAT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.		
GAM1032	CTSK	CTAGACTG AAGCTCC TTGAGGA	CTSK (Accession NM_000396.2) is another GAM1032 target gene. CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1032 RNA are set forth in Tables 6 and 7, hereby incorporated herein. Another function of GAM1032 is therefore inhibition of CTSK. Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.	A	A
GAM1032	MPO	CTAGACTG AAGCTCC TTGAGGA	Myeloperoxidase (MPO, Accession NM_000250.1) is another GAM1032 target gene. MPO BINDING SITE1 and MPO BINDING SITE2 are target binding sites found in	A	A

untranslated regions of mRNA encoded by MPO, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MPO BINDING SITE1 and MPO BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM1032 RNA are set forth in Tables 6 and 7, hereby incorporated herein. Another function of GAM1032 is therefore inhibition of MPO, a GAM1032 target gene which is present in primary granules of neutrophilic granulocytes. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MPO.The function of MPO has been established by previous studies. Weil et al. (1988) found that the MPO gene was translocated to chromosome 15 in all cases of acute promyelocytic leukemia (subtype M3), which is consistently associated with the chromosomal translocation t(15;17)(q22;q11.2). In 2 of 4 cases examined by genomic blot analysis, rearrangement of the MPO gene was detected in leukemia cells. Weil et al. (1988) also suggested that MPO may be pivotal in the pathogenesis of APL. According to HGM10, the MPO gene is located at a distance from the breakpoint in APL, and the gene itself is probably usually not rearranged in APL. Myeloperoxidase has been detected in activated microglial macrophages and

within amyloid plaques in the central nervous system. Using statistical analysis, Reynolds et al. (2000) examined the relationship between APOE (OMIM Ref. No. 107741) and MPO polymorphisms in the risk of Alzheimer disease (AD; 104300) in a genetically homogeneous Finnish population. They found that the presence of the MPO A allele in conjunction with APOE E4 significantly increased the risk of AD in men, but not in women (odds ratio for men with both alleles = 11.4 vs APOE E4 alone = 3.0). Reynolds et al. (2000) also found that estrogen receptor- alpha (OMIM Ref. No. 133430) binds to the MPO A promoter, which may explain the gender differences. Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference: Reynolds, W. F.; Hiltunen, M.; Pirskanen, M.; Mannermaa, A.; Helisalmi, S.; Lehtovirta, M.; Alafuzoff, I.; Soininen, H. : MPO and APOE epsilon- 4 polymorphisms interact to increase risk for AD in Finnish males. Neurology 55: 1284- 1290, 2000. ; an Weil, S. C.; Rosner, G. L.; Reid, M. S.; Chisholm, R. L.; Lemons, R. S.; Swanson, M. S.; Carrino, J. J.; Diaz, M. O.; Le Beau, M. M. : Translocation and rearrangement of myeloperoxida Further studies establishing the function and utilities of MPO are found in John Hopkins OMIM database record ID 606989, and in cited publications listed in Table 9, hereby incorporated

herein.

GAM1032	SERPINA 3	CTAGACTG AAGCTCC TTGAGGA	Serine (or cysteine) Proteinase Inhibitor, Clade A (alpha- 1 antiprotei (SERPINA3, Accession NM_001085.2) is another GAM1032 target gene. SERPINA3 BINDING SITE1 and SERPINA3 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by SERPINA3, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SERPINA3 BINDING SITE1 and SERPINA3 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM1032 RNA are set forth in Tables 6 and 7, hereby incorporated herein. Another function of GAM1032 is therefore inhibition of SERPINA3, a GAM1032 target gene which is a member of the serpin family of serine protease inhibitors. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SERPINA3.The function of SERPINA3 has been established by previous studies. Alpha- 1- antichymotrypsin is a plasma protease inhibitor synthesized in the liver. It is a single glycopeptide chain of about 68,000 daltons and belongs to the class of serine protease inhibitors. In man, the normal serum level is about one- tenth that of alpha- 1- antitrypsin (PI; 107400), with which it	A	A

shares nucleic acid and protein sequence homology (Chandra et al. 1983). Both are major acute phase reactants; their concentrations in plasma increase in response to trauma, surgery, and infection. Antithrombin III, which also is structurally similar to alpha- 1- antitrypsin, shows less sequence homology to antichymotrypsin and is not an acute phase reactant. Kelsey et al. (1988) cloned and analyzed the AACT gene, partly because of the possibility that genetic variation in other protease inhibitors may influence the prognosis in AAT deficiency. They isolated the AACT gene on a series of cosmid clones, with restriction mapping of about 70 kb around the gene. Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Chandra, T.; Stackhouse, R.; Kidd, V. J.; Robson, K. J. H.; Woo, S. L. C. : Sequence homology between human alpha- 1- antichymotrypsin, alpha- 1- antitrypsin, and antithrombin III. Biochemistry 22: 5055- 5061, 1983. ; an Kelsey, G. D.; Abeliovich, D.; McMahon, C. J.; Whitehouse, D.; Corney, G.; Povey, S.; Hopkinson, D. A.; Wolfe, J.; Mieli- Vergani, G.; Mowat, A. P. : Cloning of the human alpha- 1 antichym Further studies establishing the function and utilities of SERPINA3 are found in John Hopkins OMIM database record ID 107280, and in cited publications listed in Table

9, hereby incorporated herein.

Studies documenting the well known correlations between GAM TARGET GENEs that are described by Fig.8 and the known gene functions and related diseases are listed in Table 9. Specifically, Table 9 describes references of GAM target genes, as set forth in SEQ ID NO:15 in Table 8.

Table 9

GAM NAME	GAM RNA SEQUENCE	TARGET	REFERENCES	GAM POS
GAM1032	CTAGACTGAAGCTCCTTGAGGA	CHAT	Barrard, B. A.; Lottspeich, F.; Braun, A.; Barde, Y. A.; Mallet,J.: cDNA cloning and complete sequence of porcine choline acetyltransferase:in vitro translation of the corresponding RNA yields an active protein. Proc.Nat. Acad. Sci. 84:9280 - 9284, 1987.	A
GAM1032	CTAGACTGAAGCTCCTTGAGGA	CHAT	Chireux, M. A.; Le Van Thai, A.; Weber, M. J.: Human choline acetyltransferasegene: localization of alternative first exons. J. Neurosci. Res. 40:427 - 438, 1995.	A
GAM1032	CTAGACTGAAGCTCCTTGAGGA	CHAT	Cohen - Haguenauer,O.; Brice, A.; Berrard, S.; Van Cong, N.; Mallet,J.; Frezal, J.: Localization of the choline acetyltransferase (CHAT)gene to human chromosome 10. Genomics 6: 374-378, 1990.	A
GAM1032	CTAGACTGAAGCTCCTTGAGGA	CHAT	Erickson, J. D.; Varoqui, H.; Schafer, M. K. - H.; Modi, W.; Diebler,M. - F.; Weihe, E.; Rand, J.; Eiden, L. E.; Bonner, T. I.; Usdin, T.B.: Functional identification of a vesicular acetylcholine transporterand its expression from a 'cholinergic' gene locus. J. Biol. Chem. 269:21929 - 21932, 1994.	A
GAM1032	CTAGACTGAAGCTCCTTGAGGA	CHAT	Misawa, H.; Ishii, K.; Deguchi, T.: Gene expression of mouse cholineacetyltransferase: alternative splicing and identification of a highlyactive promoter region. J. Biol. Chem. 267:	A

			20392 - 20399, 1992.	
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GAM1032	CTAGAC TGAAGC TC CTTGAG GA	MPO	van Tuinen, P.; Johnson, K. R.; Ledbetter, S. A.; Nussbaum, R.L.; Rovera, G.; Ledbetter, D. H.: Localization of myeloperoxidaseto the long arm of human chromosome 17: relationship to the 15;17translocation of acute promyelocytic leukemia. Oncogene 1: 319 - 322,1987.	A
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GAM1032	CTAGACTGAAGCTCCTTGAGGA	SERPINA3	Morgan, K.; Licastro, F.; Tilley, L.; Ritchie, A.; Morgan, L.;Pedrini, S.; Kalsheker, N.: Polymorphism in the alpha - 1 - antichymotrypsin(ACT) gene promoter: effect on expression in transfected glial andliver cell lines and plasma ACT concentrations. Hum. Genet. 109:303 - 310, 2001.	A
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GAM1032	CTAGACTGAAGCTCCTTGAGGA	SERPINA3	Munoz, E.; Obach, V.; Oliva, R.; Marti, M. J.; Ezquerra, M.; Pastor,P.; Ballesta, F.; Tolosa, E.: Alpha - 1 - antichymotrypsin gene polymorphismand susceptibility to Parkinson's disease. Neurology 52: 297 - 301,1999.	A
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GAM1032	CTAGACTGAAGCTCCTTGAGGA	SERPINA3	Samilchuk, E. I.; Chuchalin, A. G.: Mis - sense mutation of alpha - 1 - antichymotrypsingene and chronic lung disease. (Letter) Lancet 342: 624, 1993.	A
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GAM1032	CTAGACTGAAGCTCCTTGAGGA	SERPINA3	Tsuda, M.; Sei, Y.; Matsumoto, M.; Kamiguchi, H.; Yamamoto, M.;Shinohara, Y.; Igarashi, T.; Yamamura, M.: Alpha - 1 - antichymotrypsinvariant detected by PCR - single strand conformation polymorphism (PCR - SSCP)and direct sequencing. Hum. Genet. 90: 467 - 468, 1992.	A
GAM1032	CTAGACTGAAGCTCCTTGAGGA	SERPINA3	Tsuda, M.; Sei, Y.; Yamamura, M.; Yamamoto, M.; Shinohara, Y.: Detection of a new mutant alpha - 1 - antichymotrypsin in patients withocclusive - cerebrovascular disease. FEBS Lett. 304: 66 - 68, 1992.	A
GAM1032	CTAGACTGAAGCTCCTTGAGGA	SERPINA3	Wang, X.; DeKosky, S. T.; Luedecking - Zimmer, E.; Ganguli, M.;Kamboh, M. I.: Genetic variation in alpha - 1 - antichymotrypsin andits association with Alzheimer's disease. Hum. Genet. 110: 356 - 365,2002.	A
GAM1032	CTAGACTGAAGCTCCTTGAGGA	SERPINA3	Yamamoto, M.; Kondo, I.; Ogawa, N.; Asanuma, M.; Yamashita, Y.;Mizuno, Y.: Genetic association between susceptibility to Parkinson's disease and alpha - 1 - antichymotrypsin polymorphism. Brain Res. 759:153 – 155, 1997.	A

Table 11 shows data relating to Alzheimer's and ALL diseases for which GAM RNA SEQ ID NO: 15 is predicted to regulate the disease-associated genes.

Table 11

ROW #	DISEASE NAME	TARGET–GENES ASSOCIATED WITH ALZHEIMER DISEASE

1	ALL	PLAU, CNTF, AVP, CRYAB, SNCB, APBA2, DHCR24, CTNND2, PSEN1, APLP1, GSK3B, APPBP2, DSCR1, MME, CRAT, AGER, NCSTN, ABCD1, BCHE, A2M, MTNR1A, APOC1, THOP1, APBA1, SERPINA3, ACHE, UBB, PIN1, TNFSF5, ADAM17, BACE2, PLCD1, APLP2, CTSK, BACE, SOD2, ADAM10, DLST, CTSG, NPY, OGDH, GYPA, PRND, CHAT, PSEN2, ACE, RAGE, GAL, APBB1, TRPM2, GSN, SNCA, BLMH, IL1A, TNFRSF6, HADH2, FHL2, ARHA, MAPK10, SLC6A4, OLR1, TGFB1, FLNB, TNF, ADAMTS5, SNCAIP, SNCG, MAPT, TFCP2, TNFRSF5, IAPP, CLU, B2M, VLDLR, GLUL, CAV2, IDE, NCKAP1, APBB2, FOS, ESR2, ACT, NGB, FPRL1, HTR2C, APCS, IGF1, CASP3, IL1B, HTR2A, GFAP, CRH, APP, SLC17A7, LRP1, PRNP, MPO, NOTCH1, S100B, MT3, CAV1, HD, BAX and CTSB.
2	Alzheimer	AVP, NCSTN, ARHA, APPBP2, HTR2A, PSEN1, DHCR24, PLAU, MTNR1A, SERPINA3, DSCR1, APBA1, APOC1, BCHE, MME, BACE2, UBB, CTNND2, APLP1, APP, SLC17A7, NCKAP1, GFAP, IGF1, SLC6A4, HD, S100B, CASP3, MPO, CNTF, GSK3B, CRH, LRP1, MT3, APBA2, CAV1, CRYAB, MAPK10, TGFB1, CHAT, TNFRSF5, CTSB, MAPT, OLR1, FLNB, CAV2, GLUL, IAPP, NGB, ACT, FOS, APBB2, TNF, SNCAIP, APLP2, PSEN2, OGDH, GYPA, ADAM17, ADAM10, ADAMTS5, BACE, TNFRSF6, ACE, HTR2C, RAGE, HADH2, FHL2, PRND, IL1A, SNCA, DLST, CTSK, TRPM2, BLMH.